

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 10, 2005, 20:48:53 ; Search time 174 Seconds
(without alignments)
915.268 Million cell updates/sec

Title: US-10-786-850-1

Perfect score: 1603

Sequence: 1 AVPSQTQWGIKSYNDQSI.....GIGAGTGDDYAGFGYPRVK 311

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 55 summaries

Database :

UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1179	73.5	431	2 Q9S3L6	Q9S3L6 bacillus sp
2	1170	73.0	434	2 O54327	O54327 bacillus sp
3	1123	70.1	416	2 Q6W4N2	Q6W4N2 bacillus sp
4	1091.5	68.1	419	2 Q45681	Q45681 bacillus su
5	1050.5	65.5	420	1 SUBT_BACSS9	P23842 bacillus sp
6	726.5	45.3	425	2 Q647R6	Q647R6 uncultured
7	477	29.8	374	2 Q9F943	Q9F943 bacillus li
8	474	29.6	310	2 Q9PDF2	Q9F943 bacillus li
9	474	29.6	310	2 Q9PDF3	Q9F943 bacillus li
10	474	29.6	374	2 Q9F941	Q9F941 bacillus li
11	474	29.6	374	2 Q9F942	Q9F942 bacillus li
12	474	29.6	379	2 Q9F943	Q9F943 bacillus mo
13	474	29.6	379	2 Q6PNN5	Q6PNN5 bacillus li
14	472	29.4	379	1 SUBT_BACLI	P00780 bacillus li
15	472	29.4	379	2 Q9PDF4	Q9F943 bacillus li
16	472	29.4	379	2 Q6SLP7	Q6SLP7 bacillus li
17	471	29.4	379	2 Q45300	Q45300 bacillus li
18	470	29.3	310	2 Q9F7C2	Q9F7C2 bacillus li
19	470	29.3	379	2 Q53521	Q53521 bacillus li
20	468	29.2	379	2 Q45301	Q45301 bacillus li
21	463.5	28.9	269	1 PRTM_BACSK	Q99405 bacillus sp
22	460	28.7	379	2 Q66153	Q66153 bacillus sp
23	458.5	28.6	404	2 Q76L29	Q76L29 bacillus sp
24	456.5	28.5	269	1 SUBS_BACLE	P23600 bacillus le
25	456.5	28.5	380	1 ELYA_BACAO	P27693 bacillus al
26	456.5	28.5	380	1 ELYA_BACCS	P41362 bacillus cl
27	455	28.4	274	1 SUBD_BACLI	P00781 bacillus li
28	454	28.3	374	2 Q45523	Q45523 bacillus sp
29	454	28.3	378	2 Q45466	Q45466 bacillus sp
30	447.5	27.9	382	2 Q45522	Q45522 bacillus sp
31	446.5	27.9	376	2 Q76KL9	Q76KL9 bacillus sp

32	446.5	27.9	382	2 Q6IT79	Q6IT79 bacillus sp
33	446	27.8	378	1 ELYA_BACYA	P20724 bacillus sp
34	445.5	27.8	269	1 SUBB_BACLE	P29599 bacillus le
35	445	27.8	379	2 Q45299	Q45299 bacillus li
36	444.5	27.7	275	2 Q9R7J4	Q9R7J4 bacillus su
37	443.5	27.7	361	1 ELYA_BACHD	P41363 bacillus ha
38	443.5	27.7	361	2 Q45521	Q45521 bacillus am
39	439.5	27.4	382	1 SUBT_BACAM	P00782 bacillus am
40	439.5	27.4	397	2 P97097	P97097 bacillus sp
41	437.5	27.3	379	2 Q45467	Q45467 bacillus sp
42	435.5	27.2	383	2 Q6SIX5	Q6SIX5 bacillus pu
43	434.5	27.1	383	2 Q9KWR4	Q9KWR4 bacillus pu
44	431.5	26.9	382	2 O87655	O87655 bacillus su
45	430	26.8	377	2 Q6L9T7	Q6L9T7 bacillus sp
46	427.5	26.7	275	2 Q93L66	Q93L66 bacillus su
47	427.5	26.7	381	2 Q84P18	Q84P18 bacillus su
48	425.5	26.5	381	1 SUBT_BACSA	P29142 bacillus st
49	425.5	26.5	381	1 SUBT_BACST	P07518 bacillus pu
50	422.5	26.4	275	1 SUBT_BACPU	P35835 bacillus su
51	422.5	26.4	381	1 SUBN_BACNA	Q847A2 bacillus su
52	422.5	26.4	381	2 Q847A2	Q847A2 bacillus su
53	421.5	26.3	381	1 SUBT_BACSU	P04189 bacillus su
54	416	26.0	384	2 Q56365	Q56365 thermoactin
55	415	25.9	401	2 Q9P993	Q9P993 pyrobaculum

ALIGNMENTS

RESULT 1

Q9S3L6	PRELIMINARY;	PRT;	431 AA.
AC	Q9S3L6;		
DT	01-MAY-2000 (TREMBLrel. 13, Created)		
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)		
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)		
DE	Fucative 36kDa protease.		
OS	Bacillus sphaericus.		
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.		
OX	NCBI_TaxID=1421;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=2297;		
RX	MEDLINE=99318657; PubMed=10388698;		
RA	Servant P., Rosso M.L., Hamon S., Poncet S., Delecluse A.,		
RA	Rapoport G.;		
RT	"Production of CryIIA and CryIIb toxins in Bacillus sphaericus		
RT	confers toxicity towards Aedes aegypti and resistant Culex		
RT	populations.";		
RL	Appl. Environ. Microbiol. 65:3021-3026(1999).		
CC	-1- SIMILARITY: Belongs to peptidase family S8.		
DR	EMBL; AJ238598; CAB46075.1; -		
DR	PDB; IEA7; X-ray; A=122-431.		
DR	MEROPS; S08.113; -		
DR	GO; GO:0008233; F:peptidase activity; IEA.		
DR	GO; GO:0004289; F:subtilase activity; IEA.		
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.		
DR	InterPro; IPR00209; Pept_S8_S53.		
DR	Pfam; PF00082; Peptidase_S8; 1.		
DR	PRINTS; PR00723; SUBTILISIN.		
DR	PROSITE; PS00136; SUBTILASE ASP; UNKNOWN_1.		
DR	PROSITE; PS00137; SUBTILASE HIS; 1.		
DR	PROSITE; PS00138; SUBTILASE_SER; 1.		
KW	Hydrolase; Protease, Serine protease.		
SQ	SEQUENCE 431 AA; 45345 MW; C1CFE8E71C2C6D2 CRC64;		

Query Match 73.5%; Score 1179; DB 2; Length 431;

Best Local Similarity 73.1%; Pred. No. 1e-69;

Matches 225; Conservative 34; Mismatches 49; Indels 0; Gaps 0;

Qy 4 STQFWGKISYNDQSIKTKGSGIKVAVLDTGYTSHLDAAGAECKDFTQSNPLVD 63

Db 124 SQQIPWGKIKYNNDTLTSTTGGSGINIAVLDTGYTSHPLVNNVECKDFTGATPIN 183

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OM protein - protein search, using sw model

Run on: September 10, 2005, 20:56:59 ; Search time 41 Seconds
(without alignments)
729,839 Million cell updates/sec

Title: US-10-786-850-1
Perfect score: 1603
Sequence: 1 AVPSQTTPWGIKSIYNDQSI.....GIGACTGDYASGFGYPRVK 311

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 55 summaries

Database : PIR_79:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1091.5	68.1	419	1 S25835	subtilisin (EC 3.4
2	1050.5	65.5	420	1 S23407	subtilisin (EC 3.4
3	472	29.4	379	1 SUBSCL	subtilisin (EC 3.4
4	466	29.1	275	2 JCI085	subtilisin (EC 3.4
5	456.5	28.5	380	2 A43778	high-alkaline seri
6	455	28.4	274	1 SUBSD	subtilisin (EC 3.4
7	454	28.3	374	2 I39781	subtilisin (EC 3.4
8	447.5	27.9	382	2 I39780	subtilisin (EC 3.4
9	446	27.8	378	2 A33973	high-alkaline seri
10	443.5	27.7	361	2 G83756	subtilisin-type al
11	439.5	27.4	382	1 SUBSN	subtilisin (EC 3.4
12	438.5	27.4	361	2 A48373	high-alkaline seri
13	425.5	26.5	381	1 SUBSS	subtilisin (EC 3.4
14	425.5	26.5	381	2 JQ1487	subtilisin (EC 3.4
15	422.5	26.4	272	2 A23624	subtilisin (EC 3.4
16	422.5	26.4	381	2 JH0778	subtilisin (EC 3.4
17	421.5	26.3	381	1 SUBSI	subtilisin (EC 3.4
18	416	26.0	384	2 J44802	alkaline proteinase
19	415	25.9	401	2 A57690	aerolysin precursor
20	409	25.5	397	2 JH0075	cysteine-dependent
21	408	25.5	279	1 SUMYTV	thermatase (EC 3.4
22	403	25.1	613	2 S75976	hypothetical prote
23	402	25.1	401	2 I39974	serine proteinase
24	398.5	24.9	534	1 J50173	alkaline proteinase
25	388.5	24.2	488	2 A11930	proteinase (import
26	384.5	24.0	525	2 G84406	halolysin (importe
27	381.5	23.8	321	1 S27501	alkaline proteinase
28	381.5	23.8	645	1 SUBSMP	serine proteinase
29	377.5	23.5	372	2 D83735	subtilisin-type al

30	373	23.3	319	2 I39866	microbial serine p
31	370.5	23.1	436	2 I39973	alkaline serine pr
32	367.5	22.9	535	2 B82358	alkaline serine pr
33	364.5	22.7	293	2 JQ0380	proteinase T (EC 3
34	360	22.5	530	2 A42605	halolysin (EC 3.4
35	357.5	22.3	440	2 H72784	probable alkaline
36	356.5	22.2	513	1 A35742	aqualysin (EC 3.4
37	354.5	22.1	326	1 C41335	microbial serine p
38	354	22.1	388	1 S22387	cuticle-degrading
39	354	22.1	519	2 S71451	halolysin R4 (EC 3
40	353	22.0	384	1 SUTIKA	endopeptidase K (E
41	345.5	21.6	615	2 A42248	protease (import
42	340	21.2	393	2 T36842	probable secreted
43	340	21.2	806	2 A41341	microbial serine p
44	338	21.1	536	2 JC7826	vacuolar subtilisi
45	337.5	21.1	409	1 S32905	serine proteinase
46	337	21.0	588	2 C83836	subtilisin-type pr
47	334.5	20.9	442	2 A69587	intracellular alka
48	334	20.8	894	2 F69730	cell wall-associat
49	333	20.8	387	2 S11985	serine proteinase
50	331	20.6	379	1 JC2142	alkaline proteinase
51	329.5	20.6	322	2 G83922	intracellular alka
52	328	20.5	757	2 C94120	subtilisin-type pr
53	326.5	20.4	323	2 I39867	microbial serine p
54	326	20.3	1448	2 A12007	Subtilase family p
55	325	20.3	591	2 A75474	serine proteinase,

ALIGNMENTS

RESULT 1

S25835

subtilisin (EC 3.4.21.62) precursor - Bacillus sp. (strain TA41)

C:Species: Bacillus sp.

C:Date: 22-Nov-1993 #sequence_revision 20-Feb-1995 #text_change 18-Jun-1999

C:Accession: S25835

R:Davall, S.; Feller, G.; Narinx, B.; Gerday, C.

Gene 119, 143-144, 1992

A:Title: Sequence of the subtilisin-encoding gene from an antarctic psychrotroph Bacil

A:Reference number: S25835; MUID:93012966; PMID:1398082

A:Accession: S25835

A:Molecule type: DNA

A:Residues: 1-419 <DAV>

A:Cross-references: EMBL:X63533; NID:G40198; PIDN:CAA45096.1; PID:G40199

C:Superfamily: subtilisin; subtilisin homology

C:Keywords: extracellular protein; hydrolase; serine proteinase

F:1-23/Domain: signal sequence #status predicted <SIG>

F:24-110/Domain: propeptide #status predicted <PRO>

F:111-419/Product: microbial serine proteinase #status predicted <MAT>

F:135-373/Domain: subtilisin homology <SPT>

P:144,184,359/Active site: Asp, His, Ser #status predicted

Query Match 68.1%; Score 1091.5; DB 1; Length 419;
Best Local Similarity 67.5%; Pred. No. 7.4e-66;
Matches 208; Conservative 41; Mismatches 58; Indels 1; Gaps 1;

Qy	4	STQTPWGIKSIYNDQSIKTGGSGIKVAVLDGTGYTSHLDAGSAECKDPTQSNPLVD 63
Db	113	SQSTPWGIKALYNNSLTSTSGGAGINIAVLDTGVTNHPDLSNNVECKDFTVGTNPTD 172
Qy	64	GSCTDRQGHGTHVAGTVLAHSGNSGQGVYVAPAKLWAYKVLGNSGSGSDIAAALRH 123
Db	173	NSCTDRQGHGTHVAGSALANGGT-GSGVGVVAPADLWAYKVLGDDSGYADDIAALRH 231
Qy	124	VADASTRGSKVINMSLGSASAKDLSIADVDYAYKGVLIIVAAAGNSGSGSNTTGFPGG 183
Db	232	AGDQATALNTKVINMSLGSSESLITNAVDYAYDKGVLIIVAAAGNSGPKFGSICYPGA 291
Qy	184	LNVAVAALENVOONTYRVADSFSSRGNPNATAGDYIIQERDIEVSARGASVESTWYGG 243
Db	292	LNVAVAALENTTQNGTYRVADFPSSRGHKKRTAGDYVIQKGDVBIAPGAAYVSTWFDGG 351

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OM protein - protein search, using sw model

Run on: September 10, 2005, 20:48:08 ; Search time 166 Seconds
(without alignments)
724.593 Million cell updates/sec

Title: US-10-786-850-1
Perfect score: 1603
Sequence: 1 AVPTQTPWGIKSIYNDQSI.....GIGAGTGDDYASGFYPRVK 311

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 55 summaries

Database : A_Geneseq_16Dec04:*
1: geneseq1980s:*
2: geneseq1990s:*
3: geneseq2000s:*
4: geneseq2001s:*
5: geneseq2002s:*
6: geneseq2003as:*
7: geneseq2003bs:*
8: geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1603	100.0	311	ADR05440	Adr05440 TY145 sub
2	1603	100.0	311	ADR05388	Adr05388 TY145 sub
3	1603	100.0	311	ADS2006	AdS2006 Bacillus
4	1603	100.0	418	ABB77095	Abb77095 Bacillus
5	1179	73.5	310	ADR05391	Adr05391 Bacillus
6	1179	73.5	310	ADR05439	Adr05439 Bacillus
7	1091.5	68.1	309	ADR05441	Adr05441 TA41 sub
8	1091.5	68.1	419	ADR05390	Adr05390 TA41 sub
9	1050.5	65.5	309	ADR05442	Adr05442 TA39 sub
10	1050.5	65.5	420	ADR05389	Adr05389 TA39 sub
11	487.5	30.4	269	4	AGG66802 Novel sub
12	479	29.9	274	2	AAW11003 Alkaline
13	477	29.8	372	6	AAE22942 Bacillus
14	476	29.7	274	2	AAW15457 Subtilisin
15	475	29.6	274	2	AAW10451 C002 muta
16	475	29.6	274	2	AAW15441 Subtilisin
17	475	29.6	274	2	AAW15447 Subtilisin
18	474.5	29.6	377	2	AAE34259 Bacillus
19	474	29.6	274	2	AAE11005 Alkaline
20	474	29.6	274	4	ABM00034 Alcalase
21	474	29.6	310	6	AAE29948 Bacillus
22	473	29.5	274	1	AAE80273 Amino aci
23	473	29.5	274	1	AAE27790 B. lichen
24	473	29.5	274	2	AAW15451 Subtilisin
25	473	29.5	274	2	AAW15454 Subtilisin

26	473	29.5	274	2	AAW00080 Alkaline
27	473	29.5	274	2	AAW24910 Carleberg
28	473	29.5	274	2	AAW08312 B. lichen
29	473	29.5	274	2	AAW82795 B. lichen
30	473	29.5	274	2	AAW08317 B. lichen
31	473	29.5	274	3	AAW02975 Bacillus
32	473	29.5	274	3	AAW77003 Bacillus
33	473	29.5	274	3	AAW03774 Subtilisin
34	473	29.5	274	3	AAW38519 Subtilisin
35	473	29.5	274	5	ABW75075 Bacillus
36	473	29.5	274	5	ABG91095 Subtilisin
37	473	29.5	274	6	ABP54392 Bacillus
38	473	29.5	274	7	ADZ25792 B. lichen
39	473	29.5	274	7	ADZ81096 Bacillus
40	473	29.5	274	7	ADF66224 B. lichen
41	473	29.5	274	8	ADH69158 B. lichen
42	473	29.5	274	8	ADJ77874 B. lichen
43	473	29.5	274	8	ADJ46871 B. lichen
44	473	29.5	274	8	ADO04602 Bacillus
45	472.5	29.5	383	5	ADE54158 L-25 kera
46	472	29.4	274	1	AAW90377 Subtilisin
47	472	29.4	274	3	AAW11907 Mature wi
48	472	29.4	274	4	AAW62485 Amino aci
49	472	29.4	274	4	AAW62487 Amino aci
50	472	29.4	274	6	ABR63751 Bacillus
51	472	29.4	274	6	ABR63735 Bacillus
52	472	29.4	274	7	ABR63726 B licheni
53	472	29.4	274	7	ABR63648 B licheni
54	472	29.4	274	7	ADC18496 Bacillus
55	472	29.4	274	7	ADD85940 Bacillus

ALIGNMENTS

RESULT 1

ADR05440 ADR05440 standard; protein; 311 AA.
XX
AC ADR05440;
XX
DT 04-NOV-2004 (first entry)
XX
DE TY145 subtilase amino acid sequence.
XX
KW Subtilisin family subtilase; subtilase; enzyme; subtilase variant;
KW three-dimensional structure; 3D structure; protein co-ordinate data;
KW Thr-Tyr145 subtilase; TY145 subtilase; ion-binding site; detergent;
KW cleaning; washing.
XX
OS Bacillus sp.
XX Synthetic.
XX
PN WO2004067737-A2.
XX
PD 12-AUG-2004.
XX
PF ADR05389 TA39 sub
XX
PR AAG66802 Novel sub
XX
PR AAR11003 Alkaline
XX
PR AAE22942 Bacillus
XX
PR AAW15457 Subtilisin
XX
PR AAR10451 C002 muta
XX
PR AAW15441 Subtilisin
XX
PR AAW15447 Subtilisin
XX
PI AAR34259 Bacillus
XX
PI AAE11005 Alkaline
XX
DR ABM00034 Alcalase
XX
PT AAE29948 Bacillus
XX
PT AAE80273 Amino aci
XX
PT AAR27790 B. lichen
XX
PT AAW15451 Subtilisin
XX
PT AAW15454 Subtilisin

Producing variant of parent Subtilisin family subtilase which are useful in washing and cleaning applications. Involves use of three-dimensional model of known subtilases for identifying and modifying parts structural parts of parent.

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OM protein - protein search, using sw model

Run on: September 10, 2005, 21:07:05 ; Search time 163 Seconds
(without alignments)
752.566 Million cell updates/sec

Title: US-10-786-850-1

Perfect score: 1603

Sequence: 1 AVPSTQTPWGIKSIYNDQSI.....GIGAGTGDYAGRGYPRVK 311

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1777461 seqs, 394431504 residues

Total number of hits satisfying chosen parameters: 1777461

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 55 summaries

Database :

Published Applications AA.*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US06_PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1603	100.0	311	16 US-10-786-850-1	Sequence 1, Appli
2	1603	100.0	418	9 US-09-966-921A-2	Sequence 2, Appli
3	1179	73.5	310	16 US-10-786-850-4	Sequence 3, Appli
4	1091.5	68.1	419	16 US-10-786-850-3	Sequence 4, Appli
5	1050.5	65.5	420	16 US-10-786-850-2	Sequence 5, Appli
6	477	29.8	372	10 US-09-813-408-9	Sequence 9, Appli
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26	472	29.4	274	17	US-10-836-959-19	Sequence 19, Appli
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43	469	29.3	276	14	US-10-243-576-31	Sequence 31, Appli
44	469	29.3	276	9	US-09-920-118-14	Sequence 14, Appli
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ALIGNMENTS

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; Sequence 1, Application US/10786850
; Publication No. US20040209343A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Draborg, Henriette
; TITLE OF INVENTION: Subtilase variants
; FILE REFERENCE: 10203
; CURRENT APPLICATION NUMBER: US/10/786.850
; CURRENT FILING DATE: 2004-02-24
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 311
; TYPE: PRT
; ORGANISM: TY145 subtilase
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(311)
US-10-786-850-1

Query Match 100.0%; Score 1603; DB 16; Length 311;
Best Local Similarity 100.0%; Pred. No. 1.8e-125;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 10, 2005, 20:58:19 ; Search time 43 Seconds
(without alignments)
539.904 Million cell updates/sec

Title: US-10-786-850-1
Perfect score: 1603
Sequence: 1 AVPSTQTPWGIKSIYNDQSI.....GIGACTGDDYASGFGYPRVK 311

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Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0*

Maximum Match 100*

Listing first 55 summaries

Database : Issued Patents AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	487.5	30.4	269	4	US-09-533-480C-2
4	474.5	29.6	377	1	US-07-772-087-2
5	473	29.5	274	1	US-08-322-677A-9
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7	473	29.5	274	2	US-09-135-658-2
8	473	29.5	274	3	US-08-898-218-9
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11	473	29.5	274	3	US-09-178-155-5
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14	473	29.5	274	4	US-09-178-173A-5
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19	473	29.5	274	4	US-10-033-325-5
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29	472	29.4	274	4	US-10-243-576-6	Sequence 6, Appli
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32	472	29.4	378	1	US-07-772-087-4	Sequence 4, Appli
33	472	29.4	379	2	US-08-845-295A-1	Sequence 1, Appli
34	472	29.4	379	3	US-09-140-933-1	Sequence 1, Appli
35	472	29.4	379	3	US-09-146-661-1	Sequence 1, Appli
36	472	29.4	379	3	US-09-150-515-1	Sequence 1, Appli
37	471	29.4	276	4	US-10-243-576-35	Sequence 35, Appli
38	470	29.3	276	4	US-10-243-576-37	Sequence 37, Appli
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40	470	29.3	379	1	US-08-685-774-2	Sequence 2, Appli
41	469	29.3	276	4	US-10-243-576-27	Sequence 27, Appli
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43	469	29.3	276	4	US-10-243-576-31	Sequence 31, Appli
44	468.5	29.2	275	6	5472855-5	Patent No. 5472855
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46	466	29.1	276	4	US-10-243-576-23	Sequence 23, Appli
47	466	29.1	276	4	US-10-243-576-25	Sequence 25, Appli
48	459.5	28.7	269	1	US-07-706-691G-50	Sequence 50, Appli
49	459.5	28.7	269	1	US-08-254-021-50	Sequence 50, Appli
50	459.5	28.7	269	2	US-08-618-446-50	Sequence 50, Appli
51	459.5	28.7	269	3	US-08-980-135-50	Sequence 50, Appli
52	459.5	28.7	269	4	US-09-585-798-50	Sequence 50, Appli
53	459.5	28.7	271	4	US-10-243-576-34	Sequence 34, Appli
54	458.5	28.6	271	4	US-10-243-576-36	Sequence 36, Appli
55	458.5	28.6	271	4	US-10-243-576-38	Sequence 38, Appli

ALIGNMENTS

RESULT 1

US-09-966-921A-2
; Sequence 2, Application US/09966921A
; Patent No. 6511371
; GENERAL INFORMATION:
; APPLICANT: Outtrup, Helle
; APPLICANT: Lassen, Soren
; APPLICANT: Pedersen, Poul
; TITLE OF INVENTION: Nucleic Acids Encoding Polypeptides Having Proteolytic Activity
; FILE REFERENCE: 10097.200-US
; CURRENT APPLICATION NUMBER: US/09/966,921A
; CURRENT FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-966-921A-2

Query Match 100.0%; Score 1603; DB 4; Length 418;
Best Local Similarity 100.0%; Pred. No. 5.7e-120;
Matches 311; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	288	PGGLVNAVAALENVQNGTYRVADFSRGNPATAGDYIIQERDIEVSAPGASVESTWY	347